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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/924,103

DATE: 10/30/2003

TIME: 14:44:36

Input Set : A:\18731055.app

Output Set: N:\CRF4\10302003\I924103.raw

3 <110> APPLICANT: GOLDENBERG, DAVID M.
4 HANSEN, HANS J.
6 <120> TITLE OF INVENTION: IMMUNOTHERAPY FOR CHRONIC MYELOCYTIC LEUKEMIA
8 <130> FILE REFERENCE: 018733-1055
10 <140> CURRENT APPLICATION NUMBER: 09/924,103
11 <141> CURRENT FILING DATE: 2001-08-08
13 <160> NUMBER OF SEQ ID NOS: 4
15 <170> SOFTWARE: PatentIn Ver. 2.1
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 2073
19 <212> TYPE: DNA
20 <213> ORGANISM: Homo sapiens
22 <400> SEQUENCE: 1

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24 taggacccca aacatctctg tgacctcctt gctgggggta aatccaacct tcccagacgt 120
25 gtgagaacac taggaacatc ctgcacacat agagggggtt ctctgtcaca gagaaaataa 180
26 caccagggtt gaggacccca gggactctct gtgtggtgct gacagaccca aggccagac 240
27 acagcagagg tccgtgctgg ggagagcggg tcgtcctgtt atggaacagg ggtccaaaca 300
28 agcttgcttc tcagagcatc ttctggggaa ctgaatataa acagaaaggg aagaggagga 360
29 gggacaaaag agacagaaat gagaggggag gggatagagg attcctgaac agagaccgca 420
30 cccatgaccc acgtgaccct gggaaatgct tctatccctg agaggaggct cagcacagaa 480
31 ggaggaagga cagcagggcc aacagtcaca gcagccctga ccagagcatt cctggagctc 540
32 aagctcctct acaaagaggt ggacagagaa gacagcagag accatgggac cccctcagc 600
33 ccctccctgc agattgcatg tcccctggaa ggaggtcctg ctcacagggt aggggaggac 660
34 tccctcggag tggatgggag gagggagcac agagactggc tagggctctc tggggaggac 720
35 aaggctctga gaggagacag agggcttttg ttgaagcctg aggaaacaga acaccagaga 780
36 gggacagggg tcacaacagg aaagtcacac taaactggga ttgataaaaa gggaggaaaa 840
37 tcaattgatc atgttttcca agttaatcat catttgctat taccatttga aaaaaagaa 900
38 aaatgataga aatcagaact gcattaggat gacactccaa ataaaaatat aacaaggaaa 960
39 ctaaatgctg cccttactca ccaatcagaa gttgaaaaat aaccaccaga tacactcatt 1020
40 aactcatcca caagcatttg caatcaattt tagtcaatgg catacaacaa gcatcagaca 1080
41 agtctcagtc atcacagagc ttatgctgtc atgaagagga aaacacacac acaaagagat 1140
42 atagaatgtg aggtcagggt ttgacaagag ccctggaagg aacagagcag ggaaaggta 1200
43 gaaagaaaag acccaggggtc tgtagagggg gtgtcaggga agggatctcc caagaatgcc 1260
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46 tgactttgac tcagtaggac acacacacac acacacacac acacgctcca 1440
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48 taggtcccaa tattgaccga tgctctctcc tctctcctag cctcacttct aaccttctgg 1560
49 aaccacacca ccaactgcaa gctcactatt gaatccacgc cattcaatgt cgcagagggg 1620
50 aaggagggtt ttctactcgc ccacaacctg cccagaatc gtattgggta cagctggta 1680
51 aaaggcgaag gagtggatgg caacagtcta attgtaggat atgtaatagg aactcaacaa 1740
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53 atccagaacg tcacccagaa tgacacagga ttctataccc tacaagtcag aaagtcagat 1860
 54 cttgtgaatg aagaagcaac cggacagttc catgtatacc gtgagtattt ccacatgacc 1920
 55 tctgggtgtt gggggtcagt tctacttccc acatacggga ttgtcaggcc tgggttgtgc 1980
 56 ctgtggccct ctctgcatta catcctgtat cagggtttgg acatttagtg caggacacac 2040
 57 acgggggaga caaacttcca cagatcagaa ttc 2073

60 <210> SEQ ID NO: 2

61 <211> LENGTH: 141

62 <212> TYPE: PRT

63 <213> ORGANISM: Homo sapiens

65 <400> SEQUENCE: 2

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69 Glu Val Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr

70 20 25 30

72 Thr Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly

73 35 40 45

75 Lys Glu Val Leu Leu Leu Ala His Asn Leu Pro Gln Asn Arg Ile Gly

76 50 55 60

78 Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Ser Leu Ile Val

79 65 70 75 80

81 Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser

82 85 90 95

84 Gly Arg Glu Thr Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Val

85 100 105 110

87 Thr Gln Asn Asp Thr Gly Phe Tyr Thr Leu Gln Val Ile Lys Ser Asp

88 115 120 125

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91 130 135 140

94 <210> SEQ ID NO: 3

95 <211> LENGTH: 1364

96 <212> TYPE: DNA

97 <213> ORGANISM: Homo sapiens

99 <400> SEQUENCE: 3

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102 cgcccaccac tgctcagctc actattgaag ctgtgccatc caatgctgca gaggggaagg 180

103 aggttcttct acttgctccac aatctgcccc aggaccctcg tggctacaac tggtagaaag 240

104 gggaaacagt ggatgccaac cgtcgaatta taggatatgt aatatcaaat caacagatta 300

105 cccagggcc tgcatacagc aatcgagaga caatataccc caatgcatcc ctgctgatgc 360

106 ggaacgtcac caaaaatgac acaggatcct acaccctaca agtcataaag ctaaattcta 420

107 tgagtgaaga agtaactggc cagttcagcg tacatccgga gactccaag ccctccatct 480

108 ccagcaacaa ctccaacccc gtggaggaca aggatgctgt ggccttcacc tgtgaacctg 540

109 agactcagaa cacaacctac ctgtggtggg taaatggtca gactctccc gtcagtcaca 600

110 ggctgcagct gtccaatggc aacaggacct tcactctact cagtgtcaca aggaatgacg 660

111 taggacccta tgaatgtgaa atacagaacc cagcgagtgc aaacttcagt gaccagtgca 720

112 ccctgaatgt cctctatggc ccagatgccc ccaccatttc cccttcagac acctattacc 780

113 atgcaggggt aaatctcaac ctctcctgcc atgcggcctc taatccaccc tcacagtatt 840

114 cttggtctgt caatggcaca ttccagcaat acacacaaaa gctctttatc cccaacatca 900

115 ctacaaagaa cagcggatcc tatgcctgcc acaccactaa ctgagccact ggccgcaaca 960

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116 ggaccacagt caggatgatc acagtctctg atgctttagt acaaggaagt tctcctggcc 1020
117 tctcagctag agccactgtc agcatcatga ttggagtact ggccagggtg gctctgatat 1080
118 agtagctctg gtgtagtttc tgcatttcaa gaagactggc agacagttgt ttttattctt 1140
119 cctcaaagca tttgcaatca gctaccattc aaaattgctt cttcttcaag atttatggaa 1200
120 aatactctga cgagtactct tgaacacaag ttcctgataa ctttaagatc acgccactgg 1260
121 actgtctatg aacttgcaaa caggctgata cctttgtgaa gttgccacc aaaacacaga 1320
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125 <210> SEQ ID NO: 4

126 <211> LENGTH: 349

127 <212> TYPE: PRT

128 <213> ORGANISM: Homo sapiens

130 <400> SEQUENCE: 4

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135           20           25           30
137 Thr Ala Gln Leu Thr Ile Glu Ala Val Pro Ser Asn Ala Ala Glu Gly
138           35           40           45
140 Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln Asp Pro Arg Gly
141           50           55           60
143 Tyr Asn Trp Tyr Lys Gly Glu Thr Val Asp Ala Asn Arg Arg Ile Ile
144   65           70           75           80
146 Gly Tyr Val Ile Ser Asn Gln Gln Ile Thr Pro Gly Pro Ala Tyr Ser
147           85           90           95
149 Asn Arg Glu Thr Ile Tyr Pro Asn Ala Ser Leu Leu Met Arg Asn Val
150           100          105          110
152 Thr Lys Asn Asp Thr Gly Ser Tyr Thr Leu Gln Val Ile Lys Leu Asn
153           115          120          125
155 Leu Met Ser Glu Glu Val Thr Gly Gln Phe Ser Val His Pro Glu Thr
156           130          135          140
158 Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Asn Pro Val Glu Asp Lys
159 145           150          155          160
161 Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asn Thr Thr Tyr
162           165          170          175
164 Leu Trp Trp Val Asn Gly Gln Ser Leu Pro Val Ser Pro Arg Leu Gln
165           180          185          190
167 Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Leu Ser Val Thr Arg Asn
168           195          200          205
170 Asp Val Gly Pro Tyr Glu Cys Glu Ile Gln Asn Pro Ala Ser Ala Asn
171           210          215          220
173 Phe Ser Asp Pro Val Thr Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
174 225           230          235          240
176 Thr Ile Ser Pro Ser Asp Thr Tyr Tyr His Ala Gly Val Asn Leu Asn
177           245          250          255
179 Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ser Gln Tyr Ser Trp Ser
180           260          265          270
182 Val Asn Gly Thr Phe Gln Gln Tyr Thr Gln Lys Leu Phe Ile Pro Asn
183           275          280          285
185 Ile Thr Thr Lys Asn Ser Gly Ser Tyr Ala Cys His Thr Thr Asn Ser

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186      290      295      300
188 Ala Thr Gly Arg Asn Arg Thr Thr Val Arg Met Ile Thr Val Ser Asp
189 305      310      315      320
191 Ala Leu Val Gln Gly Ser Ser Pro Gly Leu Ser Ala Arg Ala Thr Val
192      325      330      335
194 Ser Ile Met Ile Gly Val Leu Ala Arg Val Ala Leu Ile
195      340      345

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